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Amendments to Claims

Claim 1. (Currently Amended) A-An isolated carotenoid overproducing *E. coli* bacteria comprising the genes encoding a functional carotenoid enzymatic biosynthetic pathway wherein the *dxs*, *idi* and *ygbBP* genes are overexpressed and wherein the *yjeR* gene is down regulated and wherein the *dxs*, *idi* and *ygbBP* and *yjeR* genes are derived from either *E. coli* or *Methylomonas*. -

Claim 2. (Currently Amended) A-An isolated carotenoid overproducing bacteria *E. coli* comprising the genes encoding a functional carotenoid enzymatic biosynthetic pathway wherein the *dxs*, *idi*, *ygbBP* and *ispB* genes are overexpressed, and wherein the *dxs*, *idi*, *ygbBP* and *ispB* genes are derived either from *E. coli* or *Methylomonas* -

Claim 3. (Currently Amended) The carotenoid overproducing bacteria-*E. coli* of Claim 1 or 2 wherein the *lytB* and *dxr* gene is optionally overexpressed and wherein the *lytB* and *dxr* genes are derived from *E. coli* or *Methylomonas*.  
*ispB*, *lytB* and *dxr*, *yjeR*

Claim 4. (Currently Amended) The carotenoid overproducing bacteria-*E. coli* of Claim 1 or 2 wherein the carotenoid enzymatic biosynthetic pathway consists of the genes *dxs*, *dxr*, *ygpP*, *ychB*, *ygbB*, *lytB*, *idi*, *ispA*, *ispB*, *crtE*, *crtB*, *crtI*, and *crtY*.

Claim 5. (Currently Amended) The carotenoid overproducing bacteria-*E. coli* of Claim 4 wherein the carotenoid enzymatic biosynthetic pathway optionally additionally comprises the *crtZ* and *crtW* genes.

Claim 6-8. (Canceled)

Claim 9. (Currently amended) The carotenoid overproducing bacteria-*E. coli* of any of Claims 1-3 of Claims 1 or 2 wherein the *dxs*, *idi*, *ispB* and *ygbBP* genes are under the control of a strong promoter.

Claim 10. (Currently Amended) The carotenoid overproducing bacteria-*E. coli* of Claim 9 wherein the strong promoter is selected from the group consisting of *lac*, *ara*, *tet*, *trp*,  $\lambda P_L$ ,  $\lambda P_R$ , *T7*, *tac*, *P<sub>T5</sub>*, and *trc*.

Claim 11. (Currently amended) The carotenoid overproducing bacteria-*E. coli* of any of Claims 1-3 either of Claims 1 or 2 wherein the *dxs*, *idi*, *ispB* and *ygbBP* genes are integrated in multicity in the bacterial chromosome.

Claim 12. (Currently amended) The carotenoid overproducing bacteria-*E. coli* of any of Claims 1-3 either of Claims 1 or 2 wherein the *dxs*, *idi*, *ispB* and *ygbBP* genes are present in multicity in the bacteria on one or more plasmids.

Claim 13. (Currently Amended) The carotenoid overproducing bacteria of Claim 17 wherein the *yjeR* gene is down regulated by gene disruption.

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Claim 14. (Currently Amended) The carotenoid overproducing bacteria *E. coli* of Claim 13 wherein the disrupted *yjeR* gene has the nucleotide sequence as set forth in SEQ ID NO:63.

Claim 15. (Currently amended) The carotenoid overproducing bacteria *E. coli* of either of ~~any of Claims 1 – 3~~ Claims 1 or 2 wherein the *dxs*, *idi*, *ispB* *ygbBP* and *lytB* genes are chromosomally integrated into the host cell genome.

Claim 16. (Currently Amended) A carotenoid overproducing bacteria *E. coli* selected from the group consisting of: a strain having the ATCC identification number PTA-4807 and a strain having the ATCC identification number PTA-4823.

Claim 17. (Withdrawn) A method for the production of a carotenoid comprising:

- a) growing the carotenoid overproducing bacteria of any of Claims 1 – 5, the bacteria overexpressing at least one gene selected from the group consisting of *dxs*, *idi* *ygbBP*, *ispB*, *lytB*, *dxr*, wherein *yjeR* is optionally downregulated, for a time sufficient to produce a carotenoid; and
- b) optionally recovering the carotenoid from the carotenoid overproducing bacteria of step (a).

Claim 18. (Withdrawn) A method according to Claim 17 wherein the carotenoid is selected from the group consisting of antheraxanthin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin,  $\beta$ -cryptoxanthin, didehydrolycopene, didehydrolycopene,  $\beta$ -carotene,  $\zeta$ -carotene,  $\delta$ -carotene,  $\gamma$ -carotene, keto- $\gamma$ -carotene,  $\psi$ -carotene,  $\epsilon$ -carotene,  $\beta,\psi$ -carotene, torulene, echinenone, gamma-carotene, zeta-carotene, alpha-cryptoxanthin, diatoxanthin, 7,8-didehydroastaxanthin, fucoxanthin, fucoxanthinol, isorenieratene,  $\beta$ -isorenieratene lactucaxanthin, lutein, lycopene, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytene, rhodopin, rhodopin glucoside, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, uriolide, uriolide acetate, violaxanthin, zeaxanthin- $\beta$ -diglucoside, zeaxanthin, and C30-carotenoids.

Claim 19. (Withdrawn) A method according to Claim 18 wherein the carotenoid is produced at a level of at least about 6 mg per gram dry cell weight.

Claim 20. (Withdrawn) A method according to Claim 18 wherein the bacteria is selected from the group consisting of *Agrobacterium*, *Erythrobacter*, *Chlorobium*, *Chromatium*, *Flavobacterium*, *Cytophaga*, *Rhodobacter*, *Rhodococcus*, *Streptomyces*, *Brevibacterium*, *Corynebacteria*, *Mycobacterium*, *Deinococcus*, *Paracoccus*, *Escherichia*, *Bacillus*, *Myxococcus*, *Salmonella*, *Yersinia*, *Erwinia*, *Pantoea*, *Pseudomonas*, *Sphingomonas*, *Methylomonas*, *Methylobacter*, *Methylococcus*, *Methylosinus*, *Methylomicrobium*, *Methylocystis*, *Alcaligenes*, *Synechocystis*, *Synechococcus*, *Anabaena*, *Thiobacillus*, *Methanobacterium*, *Klebsiella*, and *Myxococcus*.

Claim 21. (Withdrawn) A method according to Claim 20 wherein the bacteria is *E. coli*.

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**Claim 22. (Withdrawn)** A method according to Claim 17 wherein the *dxs*, *idi*, *ygbBP*, *ispB* and *lytB* genes are under the control of a promoter selected from the group consisting of *lac*, *ara*, *tet*, *tRP*,  $\lambda P_L$ ,  $\lambda P_R$ , *T7*, *tac*, *P<sub>T5</sub>*, and *trc*.

**Claim 23. (Withdrawn)** A method according to Claim 17 wherein the *dxs*, *idi*, *ispB*, *ygbBP* and *lytB* genes are integrated in multicopy in the bacterial chromosome.

**Claim 24. (Withdrawn)** A method according to Claim 17 wherein the *dxs*, *idi*, *ispB*, *ygbBP* and *lytB* genes are in multicopy in the bacteria on one or more plasmids.

**Claim 25. (Withdrawn)** A method according to Claim 17 wherein the *yjeR* gene is down regulated by gene disruption.

**Claim 26. (Withdrawn)** A method according to Claim 25 wherein the disrupted *yjeR* gene has the nucleotide sequence as set forth in SEQ ID NO:63.

**Claim 27. (Withdrawn)** A method according to Claim 17 wherein the *dxs*, *idi*, *ispB*, *ygbBP* and *lytB* genes are chromosomally integrated into the host cell genome.